

10/586229

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SEQUENCE LISTING

<110> VOLLMERS, Heinz Peter
MUELLER-HERMELINK, Hans Konrad
HENSEL, Frank

<120> Neoplasm-Specific Polypeptides and Their
Uses

<130> 50274/021003

<150> PCT/US05/02480

<151> 2005-01-26

<150> US 10/764,730

<151> 2004-01-26

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Thr Leu Thr Ala Asp Lys Ser Ser Thr Ala Tyr Met Gln Leu Ser
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 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
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 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
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tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa 144
 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
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ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc 288
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Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
50 55 60
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
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Gly Gly Gly Thr Lys Leu Glu Ile Lys
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gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt 144
Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
35 40 45

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65 70 75 80

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115	120	125	
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145	150	155	160
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Ser Asp Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp			
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Asp Arg Glu Arg Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val			
180	185	190	
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Tyr Lys Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys			
195	200	205	
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Cys Arg Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr			
210	215	220	
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Lys Val Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys			
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Tyr Arg Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu			
245	250	255	
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Ser Tyr Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln			
260	265	270	
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Val Ser Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu			
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Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly			
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Glu Ile Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu			
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His Cys Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met			
325	330	335	
aac tgc cag cag gcg ctt caa aca ctg att cag gag act gac cct ggt			1056
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340	345	350	
gca gat tac cgc att gat cga gct ttg aat gaa gct tgt gaa tct gta			1104
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355	360	365	
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Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu			
370	375	380	
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Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys			
385	390	395	400
gaa cac cgt ctc tta gag ctg cag tat ttc atc tcc cgg gat tgg aag			1248
Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys			
405	410	415	
ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt			1296
Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu			
420	425	430	
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Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly			
435	440	445	
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465	470	475	480
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His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys			
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Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly			
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Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu			
515	520	525	
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Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile			
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ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met	565	570	575		1728
gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys	580	585	590		1776
gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg	595	600	605		1824
ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu	610	615	620		1872
tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg Cys Pro Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr	625	630	635	640	1920
acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser	645	650	655		1968
ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu	660	665	670		2016
gac atc cgc ttg gag cca gat cta tac gaa gcc tgc aag agt gac atc Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile	675	680	685		2064
aaa aac ttc tgt tcc gct gtg caa tat ggc aac gct cag att atc gaa Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu	690	695	700		2112
tgt ctg aaa gaa aac aag aag cag cta agc acc cgc tgc cac caa aaa Cys Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys	705	710	715	720	2160
gta ttt aag ctg cag gag aca gag atg atg gac cca gag cta gac tac Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr	725	730	735		2208
acc ctc atg agg gtc tgc aag cag atg ata aag aag ttc tgt ccg gaa Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu	740	745	750		2256
gca gat tct aaa acc atg ttg cag tgc ttg aag caa aat aaa aac agt Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser	755	760	765		2304
gaa ttg atg gat ccc aaa tgc aaa cag atg ata acc aag cgc cag atc					2352

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770					775					780								
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Thr	Gln	Asn	Thr	Asp	Tyr	Arg	Leu	Asn	Pro	Met	Leu	Arg	Lys	Ala	Cys			
785					790					795					800			
aaa	gct	gac	att	cct	aaa	ttc	tgt	cac	ggt	atc	ctg	act	aag	gcc	aag	2448		
Lys	Ala	Asp	Ile	Pro	Lys	Phe	Cys	His	Gly	Ile	Leu	Thr	Lys	Ala	Lys			
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gat	gat	tca	gaa	tta	gaa	gga	caa	gtc	atc	tct	tgc	ctg	aag	ctg	aga	2496		
Asp	Asp	Ser	Glu	Leu	Glu	Gly	Gln	Val	Ile	Ser	Cys	Leu	Lys	Leu	Arg			
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tat	gct	gac	cag	cgc	ctg	tct	tca	gac	tgt	gaa	gac	cag	atc	cga	atc	2544		
Tyr	Ala	Asp	Gln	Arg	Leu	Ser	Ser	Asp	Cys	Glu	Asp	Gln	Ile	Arg	Ile			
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att	atc	cag	gag	tcc	gcc	ctg	gac	tac	cgc	ctg	gat	cct	cag	ctc	cag	2592		
Ile	Ile	Gln	Glu	Ser	Ala	Leu	Asp	Tyr	Arg	Leu	Asp	Pro	Gln	Leu	Gln			
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ctg	cac	tgc	tca	gac	gag	atc	tcc	agt	cta	tgt	gct	gaa	gca	gca	gca	2640		
Leu	His	Cys	Ser	Asp	Glu	Ile	Ser	Ser	Leu	Cys	Ala	Glu	Glu	Ala	Ala			
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gcc	caa	gag	cag	aca	ggt	cag	gtg	gag	gag	tgc	ctc	aag	gtc	aac	ctg	2688		
Ala	Gln	Glu	Gln	Thr	Gly	Gln	Val	Glu	Glu	Cys	Leu	Lys	Val	Asn	Leu			
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ctc	aag	atc	aaa	aca	gaa	ttg	tgt	aaa	aag	gaa	gtg	cta	aac	atg	ctg	2736		
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aag	gaa	agc	aaa	gca	gac	atc	ttt	gtt	gac	ccg	gta	ctt	cat	act	gct	2784		
Lys	Glu	Ser	Lys	Ala	Asp	Ile	Phe	Val	Asp	Pro	Val	Leu	His	Thr	Ala			
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tgt	gcc	ctg	gac	att	aaa	cac	cac	tgc	gca	gcc	atc	acc	cct	ggc	cgc	2832		
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ggg	cgt	caa	atg	tcc	tgt	ctc	atg	gaa	gca	ctg	gag	gat	aag	cgg	gtg	2880		
Gly	Arg	Gln	Met	Ser	Cys	Leu	Met	Glu	Ala	Leu	Glu	Asp	Lys	Arg	Val			
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Trp	Ser	Tyr	Ala	Ala	Lys	Val	Ala	Pro	Ala	Asp	Gly	Phe	Ser	Asp	Leu			
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gcc	atg	caa	gta	atg	acg	tct	cca	tct	aag	aac	tac	att	ctc	tct	gtg	3024		
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Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly
1010 1015 1020

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340	345	350	
Ala Asp Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val			
355	360	365	
Ile Gln Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu			
370	375	380	
Ser Cys Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys			
385	390	395	400
Glu His Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys			
405	410	415	
Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu			
420	425	430	
Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly			
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Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln			
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Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu			
465	470	475	480
His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys			
485	490	495	
Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly			
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Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu			
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Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile			
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Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn			
545	550	555	560
Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met			
565	570	575	
Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys			
580	585	590	
Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg			
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Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu			
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Cys Pro Asn Ile Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr			
625	630	635	640
Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser			
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Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu			
660	665	670	
Asp Ile Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile			
675	680	685	
Lys Asn Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu			
690	695	700	
Cys Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys			
705	710	715	720
Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr			
725	730	735	
Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys Pro Glu			
740	745	750	
Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser			
755	760	765	

Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile
 770 775 780
 Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys
 785 790 795 800
 Lys Ala Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys
 805 810 815
 Asp Asp Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg
 820 825 830
 Tyr Ala Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile
 835 840 845
 Ile Ile Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln
 850 855 860
 Leu His Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala
 865 870 875 880
 Ala Gln Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu
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 Lys Glu Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala
 915 920 925
 Cys Ala Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg
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 Gly Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val
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 Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met
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 Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val
 995 1000 1005
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 35 40 45
 Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro
 50 55 60
 Gln Leu Pro Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln
 65 70 75 80
 Gln Gln Gln Pro Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly
 85 90 95
 Pro Pro Arg Arg Gly Gly Ala Gly Gly Gly Trp Lys Leu Ala
 100 105 110
 Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys His

115	120	125
Thr Trp Ser Asn Asn Leu Ala Val	Leu Glu Cys Leu Gln Asp Val Arg	
130	135	140
Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His	Leu Leu Trp Asn	
145	150	155
Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala Arg		160
165	170	175
Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp Glu		
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Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg Gly		
195	200	205
Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr Ala		
210	215	220
Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp Cys		
225	230	235
Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly Glu		240
245	250	255
Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys Gly		
260	265	270
Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser Glu		
275	280	285
Leu Cys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp Asp		
290	295	300
Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg Glu		
305	310	315
Arg Phe Cys Glu Asn Thr Gln Ala Cys Glu Gly Arg Val Tyr Lys Cys		320
325	330	335
Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg Glu		
340	345	350
Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys Val Ser		
355	360	365
Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Lys Tyr Arg Cys		
370	375	380
Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu Ser Tyr Leu		
385	390	395
Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln Val Ser Ser		400
405	410	415
Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu Met Glu Asp		
420	425	430
Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly Glu Ile Glu		
435	440	445
His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu His Cys Leu		
450	455	460
Met Lys Val Val Arg Gly Glu Lys Cys Asn Leu Gly Met Asn Cys Gln		
465	470	475
Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly Ala Asp Tyr		480
485	490	495
Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val Ile Gln Thr		
500	505	510
Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Ser Ser Cys Leu		
515	520	525
Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His Arg		
530	535	540
Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp Pro		
545	550	555
Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His Thr		560
565	570	575

His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val Phe
 580 585 590
 Ser Cys Leu Tyr Arg Glu Ala Tyr Arg Thr Glu Glu Gln Gly Arg Arg
 595 600 605
 Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu His Gln Arg
 610 615 620
 Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile
 625 630 635 640
 Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu
 645 650 655
 Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg Asp
 660 665 670
 Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile Glu
 675 680 685
 Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Thr Phe Cys His
 690 695 700
 Asp Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys Leu Ile
 705 710 715 720
 Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val
 725 730 735
 Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys
 740 745 750
 Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile
 755 760 765
 Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn
 770 775 780
 Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg
 785 790 795 800
 Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg Leu
 805 810 815
 Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn Phe Cys
 820 825 830
 Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu Lys Glu
 835 840 845
 Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe Lys Leu
 850 855 860
 Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu Met Arg
 865 870 875 880
 Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp Ser Lys
 885 890 895
 Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu Met Asp
 900 905 910
 Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln Asn Thr
 915 920 925
 Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala Asp Ile
 930 935 940
 Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu
 945 950 955 960
 Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln
 965 970 975
 Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu
 980 985 990
 Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser
 995 1000 1005
 Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln Glu Gln
 1010 1015 1020
 Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys

1025	1030	1035	1040
Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser Lys			
1045	1050	1055	
Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala Leu Asp			
1060	1065	1070	
Ile Lys His His Cys Ala Ala Leu Thr Pro Gly Arg Gly Arg Gln Met			
1075	1080	1085	
Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu Gln Pro			
1090	1095	1100	
Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser Tyr Ala			
1105	1110	1115	1120
Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met Gln Val			
1125	1130	1135	
Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser Gly Ser			
1140	1145	1150	
Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile Thr Lys			
1155	1160	1165	
Arg Val Thr Arg Glu Leu Lys Asp Arg			
1170	1175		

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<212> PRT
<213> Homo sapiens

<400> 8			
Met Ala Ala Cys Gly Arg Val Arg Arg Met Phe Arg Leu Ser Ala Ala			
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Leu His Leu Leu Leu Phe Ala Ala Gly Ala Glu Lys Leu Pro Gly			
20	25	30	
His Gly Val His Ser Gln Gly Gln Gly Pro Gly Ala Asn Phe Val Ser			
35	40	45	
Phe Val Gly Gln Ala Gly Gly Gly Pro Ala Gly Gln Gln Leu Pro			
50	55	60	
Gln Leu Leu Gln Ser Ser Gln Leu Gln Gln Gln Gln Gln Gln Gln			
65	70	75	80
Gln Gln Gln Leu Gln Pro Pro Gln Pro Pro Phe Pro Ala Gly Gly			
85	90	95	
Pro Pro Ala Arg Arg Gly Gly Ala Gly Gly Gly Trp Lys Leu			
100	105	110	
Ala Glu Glu Glu Ser Cys Arg Glu Asp Val Thr Arg Val Cys Pro Lys			
115	120	125	
His Thr Trp Ser Asn Asn Leu Ala Val Leu Glu Cys Leu Gln Asp Val			
130	135	140	
Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu Leu Trp			
145	150	155	160
Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser Val Ala			
165	170	175	
Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Lys Glu Cys Ala Asp			
180	185	190	
Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp His Arg			
195	200	205	
Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys Met Thr			
210	215	220	
Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met Asp Asp			
225	230	235	240

Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg Leu Gly
 245 250 255
 Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu Glu Lys
 260 265 270
 Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser
 275 280 285
 Glu Leu Cys Lys Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp
 290 295 300
 Asp Phe His Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg
 305 310 315 320
 Glu Arg Phe Cys Glu Asn Thr Gln Ala Arg Glu Gly Arg Val Tyr Lys
 325 330 335
 Cys Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg
 340 345 350
 Glu Ala Leu Thr Thr Arg Gln Lys Leu Ile Ala Gln Asp Tyr Lys Val
 355 360 365
 Ser Tyr Ser Leu Ala Lys Ser Cys Lys Ser Asp Leu Lys Tyr Arg
 370 375 380
 Cys Asn Val Glu Asn Leu Pro Arg Ser Arg Glu Ala Arg Leu Ser Tyr
 385 390 395 400
 Leu Leu Met Cys Leu Glu Ser Ala Val His Arg Gly Arg Gln Val Ser
 405 410 415
 Ser Glu Cys Gln Gly Glu Met Leu Asp Tyr Arg Arg Met Leu Met Glu
 420 425 430
 Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu Ser Cys Arg Gly Glu Ile
 435 440 445
 Glu His His Cys Ser Gly Leu His Arg Lys Gly Arg Thr Leu His Cys
 450 455 460
 Leu Met Lys Val Val Arg Gly Glu Lys Gly Asn Leu Gly Met Asn Cys
 465 470 475 480
 Gln Gln Ala Leu Gln Thr Leu Ile Gln Glu Thr Asp Pro Gly Ala Asp
 485 490 495
 Tyr Arg Ile Asp Arg Ala Leu Asn Glu Ala Cys Glu Ser Val Ile Gln
 500 505 510
 Thr Ala Cys Lys His Ile Arg Ser Gly Asp Pro Met Ile Leu Ser Cys
 515 520 525
 Leu Met Glu His Leu Tyr Thr Glu Lys Met Val Glu Asp Cys Glu His
 530 535 540
 Arg Leu Leu Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp
 545 550 555 560
 Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His
 565 570 575
 Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val
 580 585 590
 Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln Gly Arg
 595 600 605
 Arg Leu Leu Asp Pro Ala Leu Gln Asp Lys Cys Leu Ile Asp Leu Gly
 610 615 620
 Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly Gln Glu Leu Glu Cys Leu
 625 630 635 640
 Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu His Gln Arg Ala
 645 650 655
 Met Asp Val Lys Gln Asp His Leu Asp Asp Leu Val Val Glu Cys Arg
 660 665 670
 Asp Ile Val Gly Asn Leu Thr Glu Leu Glu Ser Glu Asp Ile Gln Ile
 675 680 685
 Glu Ala Leu Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn Phe Cys

690	695	700
His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met Glu Cys		
705	710	715
Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys Ala Ile		720
725	730	735
Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg Phe Ser		
740	745	750
Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro		
755	760	765
Asn Ile Lys Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val		
770	775	780
Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys		
785	790	795
Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile		800
805	810	815
Arg Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn		
820	825	830
Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys Leu		
835	840	845
Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys Val Phe		
850	855	860
Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp Tyr Thr Leu		
865	870	875
Met Arg Val Cys Lys Gln Met Ile Lys Arg Phe Cys Pro Glu Ala Asp		880
885	890	895
Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn Lys Asn Ser Glu Leu		
900	905	910
Met Asp Pro Lys Cys Lys Gln Met Ile Thr Lys Arg Gln Ile Thr Gln		
915	920	925
Asn Thr Asp Tyr Arg Leu Asn Pro Met Leu Arg Lys Ala Cys Lys Ala		
930	935	940
Asp Ile Pro Lys Phe Cys His Gly Ile Leu Thr Lys Ala Lys Asp Asp		
945	950	955
Ser Glu Leu Glu Gly Gln Val Ile Ser Cys Leu Lys Leu Arg Tyr Ala		960
965	970	975
Asp Gln Arg Leu Ser Ser Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile		
980	985	990
Gln Glu Ser Ala Leu Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His		
995	1000	1005
Cys Ser Asp Glu Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln		
1010	1015	1020
Glu Gln Thr Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys		
1025	1030	1035
Ile Lys Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu		1040
1045	1050	1055
Ser Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala		
1060	1065	1070
Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg Gly Arg		
1075	1080	1085
Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val Arg Leu		
1090	1095	1100
Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu Met Trp Ser		
1105	1110	1115
Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser Asp Leu Ala Met		1120
1125	1130	1135
Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile Leu Ser Val Ile Ser		
1140	1145	1150

Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly Leu Met Cys Gly Arg Ile
1155 1160 1165
Thr Lys Arg Val Thr Arg Glu Leu Lys Asp Arg
1170 1175

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<213> Artificial Sequence

<220>
<223> Primer

<400> 9
gcttggagaa aggacctggtg aa 22

<210> 10
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10
tggcacttgc ggtacaggac ag 22

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 11
gcagcttcag cagcaacagc a 21

<210> 12
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 12
cagctcagcc accccggagaa tg 22

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 13
gcttggagaa aggctggtg aa 22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
tggcacttgc ggtacaggac ag 22

<210> 15
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gaacaccgtc tcttagagct gc 22

<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 16
gcttcctgca gagtgtcatt gc 22

<210> 17
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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 17
ggaggacgtg ttgaagcttt gc 22

<210> 18
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<220>
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<400> 18

ccagggcaca agcagtatga ag	22
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caacagcaga caggtcaggt gg	22
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 gtggaaggac tcatgaccac agtc 24

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 <400> 25
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 <400> 26
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 Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
 1 5 10 15

 tat ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg 96
 Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
 20 25 30

 gtg gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc 144
 Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
 35 40 45

 gtg aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg 192
 Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
 50 55 60

 tat ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac 240
 Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
 65 70 75 80

 tgt gcg agg tcg act acg agg tct tat cct cta tac ggt atg gac gtt 288
 Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
 85 90 95

tgg ggc caa ggg aac cct gtc acc		312
Trp Gly Gln Gly Asn Pro Val Thr		
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Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro		
1 5 10 15		
gga cag acg gcc agt att acc tgt ggg gga aat aac att gga agt aaa	96	
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys		
20 25 30		
agt gtg cac tgg tac cat cag aag cca ggc cag gcc cct gtg ctg gtc	144	
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val		
35 40 45		
gtc tat gat gat agc gac cgg ccc tca ggg atc cct gag cga ttc tct	192	
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser		
50 55 60		
ggc tcc aac tct ggg aac acg gcc acc ctg acc atc acc agg gtc gaa	240	
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu		
65 70 75 80		
gcc ggg gat gag gcc gac tat tac tgt cag gtg tgg gat agt agt agt	288	
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser		
85 90 95		
gat ctc aat tgg gtg ttc ggc gga agg acc caa gct gac cgt cct acg	336	
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr		
100 105 110		
tca gcc caa ggc tgc ccc tcc ggt cac tct gtt ccc cgc ccc cct ctg	384	
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu		
115 120 125		
aag agc ttc aag ctt	399	
Lys Ser Phe Lys Leu		
130		

<210> 28		
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<213> Homo sapiens		

<400> 28
Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser
1 5 10 15
Tyr Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp
20 25 30
Val Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser
35 40 45
Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu
50 55 60
Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr
65 70 75 80
Cys Ala Arg Ser Thr Thr Arg Ser Tyr Pro Leu Tyr Gly Met Asp Val
85 90 95
Trp Gly Gln Gly Asn Pro Val Thr
100

<210> 29
<211> 133
<212> PRT
<213> Homo sapiens

<400> 29
Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro
1 5 10 15
Gly Gln Thr Ala Ser Ile Thr Cys Gly Gly Asn Asn Ile Gly Ser Lys
20 25 30
Ser Val His Trp Tyr His Gln Lys Pro Gly Gln Ala Pro Val Leu Val
35 40 45
Val Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg Phe Ser
50 55 60
Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Thr Arg Val Glu
65 70 75 80
Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Ser Ser
85 90 95
Asp Leu Asn Trp Val Phe Gly Gly Arg Thr Gln Ala Asp Arg Pro Thr
100 105 110
Ser Ala Gln Gly Cys Pro Ser Gly His Ser Val Pro Arg Pro Pro Leu
115 120 125
Lys Ser Phe Lys Leu
130

<210> 30
<211> 22
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<220>
<223> Primer

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caagagcaga caggtcaggt gg